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SEQUENCE LISTING

<110> University of Iowa Research Foundation et al.

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<120> Novel polypeptides and methods of their use

<130> 875.006WO1

10 <150> US 60/105,575

<151> 1998-10-26

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gcagaagttac	acggctatgc	cgggttgc	actgagcttc	ttgtgcatttgc	acatctcccg	6180
25gcctggtcg	tacgtcatgc	tcaacccgc	cggtgcgc	atgcccagca	gcgttgc	6240
gaaggcctgc	aagacgttgg	cagcaactggc	cggttgc	tcaggcagct	tgaccagcat	6300
caccagccgg	ctggtgcgtt	ccaccaaggt	cccgaactgc	ctggcattgc	cttctccctt	6360
gatgagatca	cttcccagt	gcccggaaa	ctggcggtct	tcgatctcg	gcgggcgtac	6420
atggatgctc	agcatgtcg	aatctggcc	tctgcggtcc	ttgccttgc	tgcggccag	6480
30ccgcttgg	ttggcgtgac	gcagggtggc	gatcagctt	ttgcgcagct	ctccacggg	6540
catggcatag	atgcagttgt	agatggttt	gtgtgacacg	cggttattcat	ggcccagggg	6600
atacaaacgt	gccagtgtca	ggcaatctg	ctcgggcgc	cagcgcagcc	gcagcagatg	6660
gatcaccagg	caggacaaga	tcgactcg	atgcagctt	atagctggtc	tgcacagcg	6720
tctgcgtgc	agggactggc	actgggcatg	tgcgtgc	tagccagatg	aagatgc	6779

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by SEQ ID NO:3

5

<400> 14

Met	Asn	Tyr	Asn	Asn	Lys	Ile	Leu	Val	Ser	Glu	Ser	Gly	Leu	Ser	Gln	
1						5				10					15	
Lys	His	Leu	Ile	His	Gly	Asp	Glu	Glu	Leu	Phe	Gln	His	Glu	Leu	Lys	
10		20					25					30				
Thr	Ile	Phe	Ala	Arg	Asn	Trp	Leu	Phe	Leu	Thr	His	Asp	Ser	Leu	Ile	
						35		40				45				
Pro	Ala	Pro	Gly	Asp	Tyr	Val	Thr	Ala	Lys	Met	Gly	Ile	Asp	Glu	Val	
		50				55				60						
15	Ile	Val	Ser	Arg	Gln	Asn	Asp	Gly	Ser	Ile	Arg	Ala	Phe	Leu	Asn	Val
65						70				75			80			
Cys	Arg	His	Arg	Gly	Lys	Thr	Leu	Val	Ser	Val	Glu	Ala	Gly	Asn	Ala	
					85				90			95				
Lys	Gly	Phe	Val	Cys	Ser	Tyr	His	Gly	Trp	Gly	Phe	Gly	Ser	Asn	Gly	
20		100					105				110					
Glu	Leu	Gln	Ser	Val	Pro	Phe	Glu	Lys	Asp	Leu	Tyr	Gly	Glu	Ser	Leu	
		115				120				125						
Asn	Lys	Lys	Cys	Leu	Gly	Leu	Lys	Glu	Val	Ala	Arg	Val	Glu	Ser	Phe	
		130				135				140						
25	His	Gly	Phe	Ile	Tyr	Gly	Cys	Phe	Asp	Gln	Glu	Ala	Pro	Pro	Leu	Met
145						150				155			160			
Asp	Tyr	Leu	Gly	Asp	Ala	Ala	Trp	Tyr	Leu	Glu	Pro	Met	Phe	Lys	His	
						165			170			175				
Ser	Gly	Gly	Leu	Glu	Leu	Val	Gly	Pro	Pro	Gly	Lys	Val	Val	Ile	Lys	
30			180				185				190					
Ala	Asn	Trp	Lys	Ala	Pro	Ala	Glu	Asn	Phe	Val	Gly	Asp	Ala	Tyr	His	
			195				200				205					
Val	Gly	Trp	Thr	His	Ala	Ser	Ser	Leu	Arg	Ser	Gly	Glu	Ser	Ile	Phe	
			210			215				220						
35	Ser	Ser	Leu	Ala	Gly	Asn	Ala	Ala	Leu	Pro	Pro	Glu	Gly	Ala	Gly	Leu
225						230				235			240			
Gln	Met	Thr	Ser	Lys	Tyr	Gly	Ser	Gly	Met	Gly	Val	Leu	Trp	Asp	Gly	
					245			250			255					
Tyr	Ser	Gly	Val	His	Ser	Ala	Asp	Leu	Val	Pro	Glu	Leu	Met	Ala	Phe	
40			260				265				270					

Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 5 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 10 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 15 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 20 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

25

<210> 15
 <211> 449
 <212> PRT
 <213> Artificial Sequence

30

<220>
 <223> A polypeptide encoded by SEQ ID NO:4

<400> 15

35 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 40 35 40 45

Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 . 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 5 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 10 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 15 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 20 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 25 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 30 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 35 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 40 355 360 365

Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 . 375 . 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 . 390 . 395 . 400
 5 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 . 410 . 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 . 425 . 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 10 . 435 . 440 . 445
 Arg

<210> 16
 15 <211> 449
 <212> PRT
 <213> Artificial Sequence

 <220>
 20 <223> A polypeptide encoded by SEQ ID NO:5

<400> 16
 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Ser Gln
 1 . 5 . 10 . 15
 25 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 . . 25 . 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 . 40 . 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 30 50 . 55 . 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 . 70 . 75 . 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 . 90 . 95
 35 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 . 105 . 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 . 120 . 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 40 130 . 135 . 140

His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 . 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 5 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 10 210 215 220
 Cys Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 15 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 20 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 25 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 30 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 35 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 17
<211> 449 .
<212> PRT
<213> Artificial Sequence
5
<220>
<223> A polypeptide encoded by SEQ ID NO:6

<400> 17
10 Met Asn Tyr Asn Asn Lys Ile Leu Val Ser Glu Phe Gly Leu Ser Gln
1 5 10 15
Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
20 25 30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
15 35 40 45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
50 55 60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
65 70 75 80
20 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
85 90 95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
100 105 110
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
25 115 120 125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
130 135 140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
145 150 155 160
30 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
165 170 175
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
180 185 190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
35 195 200 205
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
210 215 220
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
225 230 235 240
40 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly

	245	250	255
	Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
	260	265	270
	Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
5	275	280	285
	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
	290	295	300
	Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
	305	310	315
			320
10	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
	325	330	335
	Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val		
	340	345	350
	Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr		
15	355	360	365
	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu		
	370	375	380
	Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro		
	385	390	395
			400
20	Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
	405	410	415
	Tyr Arg Ala Tyr Arg Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
	420	425	430
	Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
25	435	440	445
	Arg		

<210> 18
 30 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 35 <223> A polypeptide encoded by SEQ ID NO:7

<400> 18
 Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 40 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Arg

	20	25	30
	Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile		
	35	40	45
	Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val		
5	50	55	60
	Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val		
	65	70	75
	Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala		
	85	90	95
10	Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly		
	100	105	110
	Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu		
	115	120	125
	Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe		
15	130	135	140
	His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met		
	145	150	155
	Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His		
	165	170	175
20	Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys		
	180	185	190
	Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His		
	195	200	205
	Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe		
25	210	215	220
	Ala Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu		
	225	230	235
	Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly		
	245	250	255
30	Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
	260	265	270
	Gly Gly Ser Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
	275	280	285
	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
35	290	295	300
	Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
	305	310	315
	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
	325	330	335
40	Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val		

145	150	155	160
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His			
165	170	175	
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys			
5	180	185	190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His			
195	200	205	
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe			
210	215	220	
10 Cys Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu			
225	230	235	240
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly			
245	250	255	
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe			
15	260	265	270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg			
275	280	285	
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn			
290	295	300	
20 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp			
305	310	315	320
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met			
325	330	335	
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Val			
25	340	345	350
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr			
355	360	365	
Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu			
370	375	380	
30 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro			
385	390	395	400
Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe			
405	410	415	
Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe			
35	420	425	430
Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp			
435	440	445	
Arg			

	85	90	95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly			
100	105	110	
Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu			
5	115	120	125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe			
130	135	140	
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Ser Leu Met			
145	150	155	160
10 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His			
165	170	175	
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys			
180	185	190	
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His			
15	195	200	205
Val Gly Trp Thr His Ala Ser Ser Leu Arg Thr Gly Glu Ser Ile Phe			
210	215	220	
Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu			
225	230	235	240
20 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly			
245	250	255	
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe			
260	265	270	
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Pro			
25	275	280	285
Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn			
290	295	300	
Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp			
305	310	315	320
30 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met			
325	330	335	
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val			
340	345	350	
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr			
35	355	360	365
Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile			
370	375	380	
Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro			
385	390	395	400
40 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe			

405	410	415
Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
420	425	430
Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
5	435	440
Arg		

<210> 20		
10	<211> 449	
	<212> PRT	
	<213> Artificial Sequence	
<220>		
15	<223> A polypeptide encoded by SEQ ID NO:9	
<400> 20		
Met Asn Tyr Lys Asn Lys Ile Leu Val Ser Glu Ser Gly Leu Thr Gln		
1	5	10
20		15
Lys His Leu Ile His Gly Gly Glu Gly Leu Phe Gln His Glu Leu Arg		
20	25	30
Ala Val Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile		
35	40	45
Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val		
25	50	60
Ile Val Ser Arg Gln Ser Asp Gly Ser Ile Arg Ala Phe Leu Asn Val		
65	70	75
Cys Arg His Arg Gly Lys Thr Leu Val Asn Ala Glu Ala Gly Asn Ala		
85	90	95
30 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly		
100	105	110
Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ser Leu		
115	120	125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe		
35	130	135
His Gly Phe Ile Tyr Ala Cys Ile Asp Gln Glu Ala Pro Ser Leu Met		
145	150	155
Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His		
165	170	175
40 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys		

	180	185	190
	Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His		
	195	200	205
	Val Gly Trp Thr His Ala Ser Ser Leu Cys Thr Gly Glu Ser Ile Phe		
5	210	215	220
	Ser Ser Leu Ala Gly Asn Ala Val Leu Pro Pro Glu Gly Ala Gly Leu		
	225	230	235
	Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly		
	245	250	255
	10 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
	260	265	270
	Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
	275	280	285
	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
15	290	295	300
	Ser Val Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
	305	310	315
	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
	325	330	335
	20 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val		
	340	345	350
	Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr		
	355	360	365
	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Ile		
25	370	375	380
	Ser Asn Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Ala Val Tyr Pro		
	385	390	395
	Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
	405	410	415
	30 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
	420	425	430
	Glu Asp Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
	435	440	445
	Arg		
35			
	<210> 21		
	<211> 449		
	<212> PRT		
40	<213> Artificial Sequence		

52202

<223> A polypeptide encoded by SEQ ID NO:10

<400> 21

5 Met Asn Tyr Lys Asn Lys Asn Leu Val Ser Glu Ser Gly Leu Thr Gln
 1 5 10 15
 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln Arg Glu Leu Glu
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 10 35 40 45
 Pro Ser Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 15 Cys Arg His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ala Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Glu Ala Leu
 20 115 120 125
 Asp Lys Lys Cys Met Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Glu Glu Ala Pro Ser Leu Lys
 145 150 155 160
 25 Asp Tyr Met Gly Asp Ala Gly Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Ile Gly Pro Pro Gly Lys Val Ile Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Thr Gly Asp Ala Tyr His
 30 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Val Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 35 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Glu Val Arg
 40 275 280 285

Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Phe Leu Thr Cys Ser Gly Val Phe Lys Val Trp His Pro Ile Asp
 305 310 315 320
 5 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Met Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Val Asp Ala Val Gln Arg Thr Val
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 10 355 360 365
 Val Ser Gln Asn Ala Lys Lys Tyr Gln Ser Arg Asp Gly Asp Leu Val
 370 375 380
 Ser Asn Leu Gly Phe Gly Gly Asp Val Tyr Gly Asp Glu Val Tyr Pro
 385 390 395 400
 15 Gly Ile Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gly Ala His Ile Ser Ser Ser Trp Ala Glu Phe
 420 425 430
 Glu Asp Val Ser Lys Asn Trp His Thr Glu Leu Ala Lys Thr Thr Asp
 20 435 440 445
 Arg

<210> 22
 25 <211> 447
 <212> PRT
 <213> Artificial Sequence

 <220>
 30 <223> A polypeptide encoded by SEQ ID NO:11

<400> 22
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 35 Leu Ile His Gly Asp Lys Glu Leu Phe Gln His Glu Leu Lys Thr Ile
 20 25 30
 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
 35 40 45
 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
 40 50 55 60

Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
 65 70 75 80
 His Arg Gly Lys Thr Leu Val His Ala Glu Ala Gly Asn Ala Lys Gly
 85 90 95
 5 Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly Glu Leu
 100 105 110
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Thr Ile Lys Lys
 115 120 125
 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
 10 130 135 140
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Thr Leu Val Asp Tyr
 145 150 155 160
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Ile Phe Lys His Ser Gly
 165 170 175
 15 Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys Ala Asn
 180 185 190
 Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His Val Gly
 195 200 205
 Trp Thr His Ala Ser Ser Leu Arg Ser Gly Gln Ser Ile Phe Thr Pro
 20 210 215 220
 Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225 230 235 240
 Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly Tyr Ser
 245 250 255
 25 Gly Val His Ser Ala Asp Leu Val Pro Glu Met Met Ala Phe Gly Gly
 260 265 270
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275 280 285
 Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn Ser Ile
 30 290 295 300
 Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305 310 315 320
 Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met Pro Glu
 325 330 335
 35 Asp Leu Lys Arg Arg Leu Ala Asp Ala Val Gln Arg Thr Val Gly Pro
 340 345 350
 Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr Glu Ser
 355 360 365
 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Leu Ile Ala Asn
 40 370 375 380

Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385 390 395 400
 Val Ala Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
 405 410 415
 5 Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala Glu Phe Glu Asn
 420 425 430
 Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
 435 440 445

10 <210> 23
 <211> 447
 <212> PRT
 <213> Artificial Sequence

15 <220>
 <223> A polypeptide encoded by SEQ ID NO:12

<400> 23

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 Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile Pro Ser
 35 40 45

25 Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Val Asp Glu Val Ile Val
 50 55 60
 Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe Leu Asn Val Cys Arg
 65 70 75 80
 His Arg Gly Lys Thr Leu Val His Thr Glu Ala Gly Asn Ala Lys Gly
 80 85 90 95
 Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly Ser Asn Gly Glu Leu
 100 105 110
 Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly Asp Ala Ile Lys Lys
 115 120 125

35 Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile Glu Ser Phe His Gly
 130 135 140
 Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro Pro Leu Ile Asp Tyr
 145 150 155 160
 Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Thr Phe Lys His Ser Gly
 40 165 170 175

Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Val Lys Ala Asn
 180 185 190
 Trp Lys Pro Phe Ala Glu Asn Phe Val Gly Asp Ile Tyr His Val Gly
 195 200 205
 5 Trp Thr His Ala Ala Ala Leu Arg Ala Gly Gln Ser Val Phe Ser Ser
 210 215 220
 Leu Ala Gly Asn Ala Lys Leu Pro Pro Glu Gly Ala Gly Leu Gln Met
 225 230 235 240
 Thr Ser Lys Tyr Gly Ser Gly Met Gly Leu Thr Trp Asp Tyr Tyr Ser
 10 245 250 255
 Gly Asn Phe Ser Ala Asp Met Val Pro Asp Leu Met Ala Phe Gly Ala
 260 265 270
 Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly Asp Val Arg Ala Arg
 275 280 285
 15 Ile Tyr Arg Ser Ile Leu Asn Gly Thr Val Phe Pro Asn Asn Ser Phe
 290 295 300
 Leu Thr Gly Ser Ala Thr Phe Lys Val Trp Asn Pro Ile Asp Glu Asn
 305 310 315 320
 Thr Thr Glu Val Trp Thr Tyr Ala Phe Val Glu Lys Asp Met Pro Glu
 20 325 330 335
 Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln Arg Ser Val Gly Pro
 340 345 350
 Ala Gly Phe Trp Glu Ser Asp Asn Glu Asn Met Glu Thr Leu Ser
 355 360 365
 25 Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp Gln Ile Ala Ser
 370 375 380
 Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys Tyr Pro Gly Val
 385 390 395 400
 Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe Tyr Arg
 30 405 410 415
 Ala Tyr Gln Ala His Ile Ser Ser Ser Asn Trp Ala Glu Phe Glu Asn
 420 425 430
 Ala Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr Thr Asp Arg
 435 440 445
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 <211> 451
 <212> PRT
 <213> Artificial Sequence

52202

<223> A polypeptide encoded by SEQ ID NO:13

<400> 24

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 Glu Leu Lys Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp
 10 35 40 45
 Ser Leu Ile Pro Ser Pro Gly Asp Tyr Val Lys Ala Lys Met Gly Val
 50 55 60
 Asp Glu Val Ile Val Ser Arg Gln Asn Asp Gly Ser Val Arg Ala Phe
 65 70 75 80
 15 Leu Asn Val Cys Arg His Arg Gly Lys Thr Ile Val Asp Ala Glu Ala
 85 90 95
 Gly Asn Ala Lys Gly Phe Val Cys Gly Tyr His Gly Trp Gly Tyr Gly
 100 105 110
 Ser Asn Gly Glu Leu Gln Ser Val Pro Phe Glu Lys Glu Leu Tyr Gly
 20 115 120 125
 Asp Ala Ile Lys Lys Cys Leu Gly Leu Lys Glu Val Pro Arg Ile
 130 135 140
 Glu Ser Phe His Gly Phe Ile Tyr Gly Cys Phe Asp Ala Glu Ala Pro
 145 150 155 160
 25 Pro Leu Ile Asp Tyr Leu Gly Asp Val Ala Trp Tyr Leu Glu Pro Thr
 165 170 175
 Phe Lys His Ser Gly Leu Glu Leu Val Gly Pro Pro Ala Lys Val
 180 185 190
 Val Val Lys Gly Asn Trp Lys Val Phe Ala Glu Asn Phe Val Gly Asp
 30 195 200 205
 Ile Tyr His Ile Gly Trp Thr His Ala Ser Ile Leu Arg Ala Gly Gln
 210 215 220
 Ala Ile Phe Ala Pro Leu Ala Gly Asn Ala Met Leu Pro Pro Glu Gly
 225 230 235 240
 35 Thr Gly Leu Gln Ala Thr Thr Lys Tyr Gly Ser Gly Ile Gly Val Ser
 245 250 255
 Leu Asp Ala Tyr Ser Gly Val Gln Ser Ala Asp Leu Val Pro Glu Met
 260 265 270
 Met Ala Phe Gly Gly Ala Lys Gln Glu Lys Leu Ala Lys Glu Ile Gly
 40 275 280 285

Asp Val Arg Ala Arg Ile Tyr Arg Ser Gln Val Asn Gly Thr Val Phe
 290 295 300
 Pro Asn Asn Cys Phe Leu Thr Gly Ala Gly Val Phe Lys Val Phe Asn
 305 310 315 320
 5 Pro Ile Asp Glu Asn Thr Thr Glu Ala Trp Thr Tyr Ala Ile Val Glu
 325 330 335
 Lys Asp Met Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ala Ala Gln
 340 345 350
 Arg Ser Val Gly Pro Ala Gly Tyr Trp Glu Ser Asp Asp Asn Asp Asn
 10 355 360 365
 Met Val Leu Ser Gln Asn Ala Lys Lys Tyr Gln Ser Ser Asn Ser Asp
 370 375 380
 Leu Ile Ala Asp Leu Gly Phe Gly Lys Asp Val Tyr Gly Asp Glu Cys
 385 390 395 400
 15 Tyr Pro Gly Val Val Ser Lys Ser Ala Phe Ser Glu Thr Asn His Arg
 405 410 415
 Gly Phe Tyr Arg Ala Tyr Gln Ala His Ile Ser Ser Asn Trp Ala
 420 425 430
 Glu Phe Glu Asn Thr Ser Arg Asn Trp His Thr Glu Leu Thr Lys Thr
 20 435 440 445
 Thr Asp Arg
 450

<210> 25
 25 <211> 2265
 <212> DNA
 <213> Pseudomonas sp.

<400> 25

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	cgcgtaatga ttgattttag ctaagaattt taacaggagg caccgggc cctagagcgt	180
	aatcaccccccc attccatctt ttttaggtga aaacatgaat tacaataata aaatcttggt	240
	aagtgaatct ggtctgagcc aaaagcacct gattcatggc gatgaagaac ttttccaaca	300
35	tgaactgaaa accatttttgc cgccggaaactg gcttttctc actcatgata gcctgattcc	360
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	gagcgtggaa gccggcaatg ccaaagggtt tggttcgcagc tatcacggct ggggcttcgg	540
	ctccaaacggg gaaactgcaga ggttccatt tgaaaaagat ctgtacggcg agtcgctcaa	600
40	taaaaaatgt ctgggttga aagaagtgc tcgcgtggag agcttccatg gtttcatcta	660

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25	cagcgattcg	tcgattaccc	agagcgcata	cttcagacgc	acaatctgtat	gttcttctg	2160
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<210> 26

30 <211> 449

<212> PRT

<213> *Pseudomonas* sp.

<400> 26

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Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys

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Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile

40 35 40 45

Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 5 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 10 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 15 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 20 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 25 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 30 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 35 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Phe
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 40 355 360 365

Ala Ser Gln Asn Gly Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 5 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 10 435 440 445
 Arg

15 <210> 27
<211> 2265
<212> DNA
<213> Artificial Sequence

20 <220>
<223> A modified DNA sequence

<400> 27

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25 cgcgtaatga ttgatttgag ctaagaattt taacaggagg caccggggc cctagagegt 180
aatcaccccc attccatctt ttttaggtga aaacatgaat tacaataata aaatcttggt 240
aagtgaatct ggtctgagcc aaaagcacct gattcatggc gatgaagaac ttttccaaca 300
tgaactgaaa accatTTTg cgccgaactg gcttttctc actcatgata gcctgattcc 360
tgccccggc gactatgtta ccgcaaaaat ggggattgac gaggtcatcg tctccggca 420
30 gaacgacggg tgcatttcgt ctTTTctgaa cgTTTggccgg catcggtggca agacgctgg 480
gagcggtggaa gccggcaatg ccaaaggtt tggggcagc tatcacggct ggggcttcgg 540
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35 cctggAACCT atgttcaagc attccggcggt tttagaactg gtccggcctc caggcaaggt 780
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	cagcgatttcg	tcgattaccc	agagcgcata	cttcagacgc	acaatctgat	ggtctttctg	2160
	tgattcagtg	accattttta	caaatggtca	ctgcaaccgc	ggtcaccatt	aatcaaagg	2220
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<210> 28

<211> 2265

<212> DNA

25 <213> Artificial Sequence

<220>

<223> A modified DNA sequence

30 <400> 28

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	cctggAACCT atgttcaagc atccccggg tttagaactg gtgcgtctc caggcaagg	780
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	catgggtgtt ttgtggacg gatattcagg tgcatacg gcagacttgg ttccggaaattt	1020
	gatggcatttcc ggaggcgcaa agcaggaaag gctgaacaaa gaaattggcg atgttgcgc	1080
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	cagcgattcg tcgattaccc agagcgcata cttcagacgc acaatctgtat ggtcttctg	2160
	tgattcgttgc accatttttca caaatggtca ctgcaaccgc ggtcaccatt aatcaaagg	2220
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 <211> 2265
 <212> DNA
 <213> Artificial Sequence

35 <220>
 <223> A modified DNA sequence

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35 tgattcagtg accatttttcaaaatggtca	ctgcaaccgc ggtcaccatt	aatcaaaggaaatgtacgttatggcaat	2220
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<211> 2265

40 <212> DNA

<213> Artificial Sequence

<220>

<223> A modified DNA sequence

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<400> 30

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cgcttactc	gtttat	tcac	caac	gtcc	gg	cc	gg	caat	gg	1980
40	cttcacatcc	gctccaa	acgt	catt	ctgc	ca	cg	gcac	gc	2040

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cagcgattcg tcgattaccc agagcgcata ctccagacgc acaatctgat ggtcttctg	2160
tgattcagt accatttta caaatggtca ctgcaaccgc ggtcaccatt aatcaaagg	2220
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cgcgtaatga ttgatttgcg ctaagaattt taacaggagg caccgggc cctagagcgt	180
aatcaccccccc attccatctt ttttaggtga aaacatgaat tacaataata aatcttgg	240
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20 tgaactgaaa accatttttgc cgccggactg gcttttctc actcatgata gcctgattcc	360
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25 taaaaaatgt ctggggttga aagaagtgc tcgcgtggag agctccatg gttcatcta	660
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gatggcattt ggaggcgcggc agcaggaaag gctgaacaaa gaaattggcg atgttgcgc	1080
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40 ggctgagttc gagcatgcct ctatgtacttgc gcatactgaa cttacgaaga ctactgatcg	1560

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5 tca	tagagcg	gttataagct	caatgaagcc	atgaacgttt	acaacgaaaa	ttttcagcaa	1860
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<211> 449
<212> PRT
<213> Artificial Sequence

20 <220>
<223> A polypeptide encoded by SEQ ID NO:27

<400> 32
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 25 Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
 20 25 30
 Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
 35 40 45
 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
 30 50 55 60
 Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
 65 70 75 80
 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
 85 90 95
 35 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
 100 105 110
 Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
 115 120 125
 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 40 130 135 140

His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 5 Ser Gly Gly Leu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 10 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 15 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 20 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 25 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Gly
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 30 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 35 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg

<210> 33
<211> 449
<212> PRT
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<220>
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Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys
20 25 30
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile
15 35 40 45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val
50 55 60
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val
65 70 75 80
20 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala
85 90 95
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly
100 105 110
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu
25 115 120 125
Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
130 135 140
His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
145 150 155 160
30 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
165 170 175
Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
180 185 190
Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
35 195 200 205
Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
210 215 220
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
225 230 235 240
40 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly

	245	250	255
	Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
	260	265	270
	Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
5	275	280	285
	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
	290	295	300
	Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
	305	310	315
10	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
	325	330	335
	Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ala		
	340	345	350
	Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr		
15	355	360	365
	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu		
	370	375	380
	Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro		
	385	390	395
20	Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
	405	410	415
	Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
	420	425	430
	Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
25	435	440	445
	Arg		
	<210> 34		
30	<211> 449		
	<212> PRT		
	<213> Artificial Sequence		
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	<400> 34		
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	20	25	30
	Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile		
	35	40	45
	Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val		
5	50	55	60
	Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val		
	65	70	75
	Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala		
	85	90	95
	10 Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly		
	100	105	110
	Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu		
	115	120	125
	Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe		
15	130	135	140
	His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met		
	145	150	155
	Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His		
	165	170	175
	20 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys		
	180	185	190
	Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His		
	195	200	205
	Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe		
25	210	215	220
	Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu		
	225	230	235
	Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly		
	245	250	255
	30 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
	260	265	270
	Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
	275	280	285
	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
35	290	295	300
	Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
	305	310	315
	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
	325	330	335
	40 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Thr		

	340	345	350
	Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asn Met	Glu Thr	
	355	360	365
	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu	Leu	
5	370	375	380
	Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val	Tyr Pro	
	385	390	395
	Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg	Gly Phe	
	405	410	415
10	Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala	Glu Phe	
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	Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr	Thr Asp	
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	Arg		
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	<211> 449		
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	20	25	30
30	Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile		
	35	40	45
	Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val		
	50	55	60
	Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val		
35	65	70	75
	Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala		
	85	90	95
	Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly		
	100	105	110
40	Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu		

	115	120	125
	Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe		
	130	135	140
	His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met		
5	145	150	155
	Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His		160
	165	170	175
	Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys		
	180	185	190
10	Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His		
	195	200	205
	Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe		
	210	215	220
	Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu		
15	225	230	235
	Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly		240
	245	250	255
	Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
	260	265	270
20	Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
	275	280	285
	Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
	290	295	300
	Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
25	305	310	315
	Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		320
	325	330	335
	Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Leu		
	340	345	350
30	Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr		
	355	360	365
	Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu		
	370	375	380
	Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro		
35	385	390	395
	Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		400
	405	410	415
	Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
	420	425	430
40	Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		

435

440

445

Arg

5 <210> 36

<211> 449

<212> PRT

<213> Artificial Sequence

10 <220>

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<400> 36

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Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys

20 25 30

Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile

35 40 45

20 Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val

50 55 60

Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val

65 70 75 80

Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala

25 85 90 95

Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly

100 105 110

Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu

115 120 125

30 Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe

130 135 140

His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met

145 150 155 160

Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His

35 165 170 175

Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys

180 185 190

Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His

195 200 205

40 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe

210	215	220
Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu		
225	230	235
Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly		
5	245	250
Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe		
260	265	270
Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg		
275	280	285
10 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn		
290	295	300
Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp		
305	310	315
Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met		
15	325	330
Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Ile		
340	345	350
Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr		
355	360	365
20 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu		
370	375	380
Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro		
385	390	395
Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe		
25	405	410
Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe		
420	425	430
Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp		
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30 Arg		

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5 <210> 38
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10 <220>
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gccgggcctc ttgcgggata tcgtcca 27

15 <210> 39
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20 <220>
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<400> 39
gttgccattt ctgcaggcat cgtggtg 27

25 <210> 40
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30 <220>
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35 gaggcacccg cggaagcttt tgtggagat gca 33

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<220>
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5 gcacccgcgg aacaatttgt gggagatgca 30

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<220>
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15 <400> 42
ccgcggaaag ctttgtggga g 21

<210> 43
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25 <400> 43
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30 <211> 23
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40 <210> 45

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10 <210> 46
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30 <400> 47
gacggatatt caggtaacca tagcgcagac ttg 33

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30 <220>
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40 <213> Artificial Sequence

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10 <213> Artificial Sequence

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15 <400> 53
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20 <212> DNA
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25 <400> 54
gaaaaggcgacg ccaatgacaa t 21

<210> 55

30 <211> 30
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35 <223> An oligonucleotide

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<212> DNA

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<223> A modified DNA sequence

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cgcgtaatga	ttgattttag	ctaagaattt	taacaggagg	cacccgggc	cctagagcgt	180
aatcaccccc	attccatctt	ttttaggtga	aaacatgaat	tacaataata	aaatcttggt	240
aagtgaatct	ggtctgagcc	aaaagcacct	gattcatggc	gatgaagaac	ttttccaaca	300
tgaactgaaa	accatTTTg	cgcggaaactg	gcttttctc	actcatgata	gcctgattcc	360
15 tgccccggc	gactatgtta	ccgcaaaaat	ggggattgac	gaggtcatcg	tctccggca	420
gaacgacgg	tcgattcgt	cttttctgaa	cgtttgcgg	catcggtgg	agacgctgg	480
gagcgtggaa	gccggcaatg	ccaaagggtt	tgtttgcagc	tatcacggct	ggggcttcgg	540
ctccaacgg	gaactgcaga	gcgttccatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
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20 cggttgcttc	gaccaggagg	cccccctct	tatggactat	ctgggtgacg	ctgcttggta	720
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caatgcggcg	ctaccacctg	aaggcgcagg	cttgcAAATG	acctccaaat	acggcagcgg	960
25 catgggtgt	ttgtgggacg	gatattcagg	tgtcatagc	gcagacttgg	ttccggaaatt	1020
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tcggatttat	cgcagccacc	tcaactgcac	cgtttccc	aacaacagca	tgctgacctg	1140
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cgctttactc	gctttatcac	caacgtccag	gccgcaatgg	acgtaaatga	caaagagcta	1980	
cttcacatcc	gctccaacgt	cattctgcac	cgggcacgac	gtggcaatca	ggtcgatgtc	2040	
ttctacgccc	ccccggaaaga	taaatggaaa	cgtggcgaag	gtggagtacg	aaaattggtc	2100	
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5	tgattcagtg	accatttta	caaatggtca	ctgcaaccgc	ggtcaccatt	aatcaaagg	2220
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	cgcgtaatga	ttgatttgag	ctaagaattt	taacaggagg	cacccgggc	cctagagcgt	180
20	aatcacccccc	attccatctt	tttttaggtga	aaacatgaat	tacaataata	aaatcttggt	240
	aagtgaatct	ggtctgagcc	aaaagcacct	gattcatgc	gatgaagaac	ttttccaaca	300
	tgaactgaaa	accattttg	cgcggactg	gcttttctc	actcatgata	gcctgattcc	360
	tgcccccggc	gactatgtt	ccgcaaaaat	ggggattgac	gaggtcatcg	tctccggca	420
	gaacgacggt	tcgattcgtg	ctttctgaa	cgtttgcgg	catcgtggca	agacgctgg	480
25	gagcgtggaa	gccggcaatg	ccaaagggtt	tgtttgcage	tatcacggct	ggggcttcgg	540
	ctccaaacgg	gaactgcaga	gcgttccatt	tgaaaaagat	ctgtacggcg	agtcgctcaa	600
	taaaaaatgt	ctgggggttga	aagaagtcgc	tcgcgtggag	agcttccatg	gcttcatcta	660
	cggttgttc	gaccaggagg	ccccctctt	tatggactat	ctgggtgacg	ctgcttggta	720
	cctggAACCT	atgttcaagc	attccggcgg	tttagaactg	gtcgttcctc	caggcaaggt	780
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	gggttggacg	cacgcgtt	cgcttcgtc	gggggagtct	atcttctcg	cgctcgctgg	900
	caatgcggcg	ctaccacctg	aaggcgcagg	cttgcataatg	acctccaaat	acggcagcgg	960
	catgggtgtg	ttgtggacg	gatattcagg	tgtgcatacg	gcagacttgg	ttccggaaatt	1020
	gatggcattt	ggaggcgc	aaagcaggaaag	gctgaacaaa	gaaattggcg	atgttcgcgc	1080
35	tcggatttat	cgcagccacc	tcaactgcac	cgtttcccg	aacaacagca	tgctgacctg	1140
	ctcggtgtt	ttcaaagtat	ggaacccgat	cgacgcaaac	accaccgagg	tctggaccta	1200
	cgccattgtc	aaaaaagaca	tgcctgagga	tctcaagcgc	cgcttggccg	actctgttca	1260
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	ttcgcaaaac	ggcaagaaat	atcaatcaag	agatagtat	ctgcttcaa	accttggttt	1380
40	cggtgaggac	gtatacggcg	acgcggtcta	tccaggcg	gtcggcaa	at cggcgatcgg	1440

cgagaccagt tatcggtt tctaccggc ttaccaggca cacgtcagca gctccaactg	1500
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ctaacagacg agtcgaccat gatgtatcaat attcaagaag acaagctggt ttccgcccac	1620
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ctgaaaagtgc gagttgagca tcaactggat ccgaaaact gggcaacag cccgaagctg	1920
cgttttactc gcttatcac caacgtccag gccgcaatgg acgtaaatga caaagagcta	1980
10 cttcacatcc gctccaaacgt cattctgcac cgggcacgac gtggcaatca ggtcgatgtc	2040
ttctacgccc cccggaaaga taaatggaaa cgtggcaag gtggagtagc aaaattggtc	2100
cagcgattcg tcgattaccc agagcgcata cttcagacgc acaatctgat ggtcttctg	2160
tgattcagtg accatttta caaatggta ctgcaaccgc ggtcaccatt aatcaaagg	2220
aatgtacgtg tatggcaat caacaagtgc ttgcataac cggtg	2265

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 <211> 449
 <212> PRT
 <213> Artificial Sequence

20

<220>
 <223> A polypeptide encoded by SEQ ID NO:56

<400> 58

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Lys His Leu Ile His Gly Asp Glu Glu Leu Phe Gln His Glu Leu Lys			
20	25	30	
Thr Ile Phe Ala Arg Asn Trp Leu Phe Leu Thr His Asp Ser Leu Ile			
30	35	40	45
Pro Ala Pro Gly Asp Tyr Val Thr Ala Lys Met Gly Ile Asp Glu Val			
50	55	60	
Ile Val Ser Arg Gln Asn Asp Gly Ser Ile Arg Ala Phe Leu Asn Val			
65	70	75	80
35 Cys Arg His Arg Gly Lys Thr Leu Val Ser Val Glu Ala Gly Asn Ala			
85	90	95	
Lys Gly Phe Val Cys Ser Tyr His Gly Trp Gly Phe Gly Ser Asn Gly			
100	105	110	
Glu Leu Gln Ser Val Pro Phe Glu Lys Asp Leu Tyr Gly Glu Ser Leu			
40	115	120	125

Asn Lys Lys Cys Leu Gly Leu Lys Glu Val Ala Arg Val Glu Ser Phe
 130 135 140
 His Gly Phe Ile Tyr Gly Cys Phe Asp Gln Glu Ala Pro Pro Leu Met
 145 150 155 160
 5 Asp Tyr Leu Gly Asp Ala Ala Trp Tyr Leu Glu Pro Met Phe Lys His
 165 170 175
 Ser Gly Gly Leu Glu Leu Val Gly Pro Pro Gly Lys Val Val Ile Lys
 180 185 190
 Ala Asn Trp Lys Ala Pro Ala Glu Asn Phe Val Gly Asp Ala Tyr His
 10 195 200 205
 Val Gly Trp Thr His Ala Ser Ser Leu Arg Ser Gly Glu Ser Ile Phe
 210 215 220
 Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 15 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 20 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 25 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Trp
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 30 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 35 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
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 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 40 435 440 445

Arg

<210> 59
 5 <211> 449
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<400> 59

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						20			25				30			
	Thr	Ile	Phe	Ala	Arg	Asn	Trp	Leu	Phe	Leu	Thr	His	Asp	Ser	Leu	Ile
						35			40				45			
20	Pro	Ala	Pro	Gly	Asp	Tyr	Val	Thr	Ala	Lys	Met	Gly	Ile	Asp	Glu	Val
	50					55			60							
	Ile	Val	Ser	Arg	Gln	Asn	Asp	Gly	Ser	Ile	Arg	Ala	Phe	Leu	Asn	Val
	65					70			75				80			
	Cys	Arg	His	Arg	Gly	Lys	Thr	Leu	Val	Ser	Val	Glu	Ala	Gly	Asn	Ala
						85			90				95			
25	Lys	Gly	Phe	Val	Cys	Ser	Tyr	His	Gly	Trp	Gly	Phe	Gly	Ser	Asn	Gly
						100			105				110			
	Glu	Leu	Gln	Ser	Val	Pro	Phe	Glu	Lys	Asp	Leu	Tyr	Gly	Glu	Ser	Leu
						115			120				125			
30	Asn	Lys	Cys	Leu	Gly	Leu	Lys	Glu	Val	Ala	Arg	Val	Glu	Ser	Phe	
	130					135			140							
	His	Gly	Phe	Ile	Tyr	Gly	Cys	Phe	Asp	Gln	Glu	Ala	Pro	Pro	Leu	Met
	145					150			155				160			
	Asp	Tyr	Leu	Gly	Asp	Ala	Ala	Trp	Tyr	Leu	Glu	Pro	Met	Phe	Lys	His
						165			170				175			
35	Ser	Gly	Gly	Leu	Glu	Leu	Val	Gly	Pro	Pro	Gly	Lys	Val	Val	Ile	Lys
						180			185				190			
	Ala	Asn	Trp	Lys	Ala	Pro	Ala	Glu	Asn	Phe	Val	Gly	Asp	Ala	Tyr	His
						195			200				205			
	Val	Gly	Trp	Thr	His	Ala	Ser	Ser	Leu	Arg	Ser	Gly	Glu	Ser	Ile	Phe
40	210					215			220							

Ser Ser Leu Ala Gly Asn Ala Ala Leu Pro Pro Glu Gly Ala Gly Leu
 225 230 235 240
 Gln Met Thr Ser Lys Tyr Gly Ser Gly Met Gly Val Leu Trp Asp Gly
 245 250 255
 5 Tyr Ser Gly Val His Ser Ala Asp Leu Val Pro Glu Leu Met Ala Phe
 260 265 270
 Gly Gly Ala Lys Gln Glu Arg Leu Asn Lys Glu Ile Gly Asp Val Arg
 275 280 285
 Ala Arg Ile Tyr Arg Ser His Leu Asn Cys Thr Val Phe Pro Asn Asn
 10 290 295 300
 Ser Met Leu Thr Cys Ser Gly Val Phe Lys Val Trp Asn Pro Ile Asp
 305 310 315 320
 Ala Asn Thr Thr Glu Val Trp Thr Tyr Ala Ile Val Glu Lys Asp Met
 325 330 335
 15 Pro Glu Asp Leu Lys Arg Arg Leu Ala Asp Ser Val Gln Arg Thr Tyr
 340 345 350
 Gly Pro Ala Gly Phe Trp Glu Ser Asp Asp Asn Asp Asn Met Glu Thr
 355 360 365
 Ala Ser Gln Asn Gly Lys Lys Tyr Gln Ser Arg Asp Ser Asp Leu Leu
 20 370 375 380
 Ser Asn Leu Gly Phe Gly Glu Asp Val Tyr Gly Asp Ala Val Tyr Pro
 385 390 395 400
 Gly Val Val Gly Lys Ser Ala Ile Gly Glu Thr Ser Tyr Arg Gly Phe
 405 410 415
 25 Tyr Arg Ala Tyr Gln Ala His Val Ser Ser Ser Asn Trp Ala Glu Phe
 420 425 430
 Glu His Ala Ser Ser Thr Trp His Thr Glu Leu Thr Lys Thr Thr Asp
 435 440 445
 Arg
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 35 <213> Artificial Sequence
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10 <220>
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gttcagcgaa cggccgggcc tgctgg

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15 <210> 62
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20 <220>
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25 <210> 63
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30 <220>
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26

35 <210> 64
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<400> 64

5 gttcagcgaa cgtggggcc tgctgg

26

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25